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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/804,515

DATE: 08/09/2004

TIME: 10:44:52

Input Set : A:\67130126.app
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3 <110> APPLICANT: YAMAGUCHI, MASAYOSHI
 5 <120> TITLE OF INVENTION: MODEL ANIMAL WITH OVEREXPRESSION OF REGUCALCIN
 7 <130> FILE REFERENCE: 671302-2006
 9 <140> CURRENT APPLICATION NUMBER: 10/804,515
 10 <141> CURRENT FILING DATE: 2004-03-19
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP02/09611
 13 <151> PRIOR FILING DATE: 2002-09-19
 15 <150> PRIOR APPLICATION NUMBER: JP 2002-177666
 16 <151> PRIOR FILING DATE: 2002-06-18
 18 <150> PRIOR APPLICATION NUMBER: JP 2001-287698
 19 <151> PRIOR FILING DATE: 2001-09-20
 21 <160> NUMBER OF SEQ ID NOS: 4
 23 <170> SOFTWARE: PatentIn Ver. 3.2
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 900
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Rattus norvegicus
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 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(897)
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 36 Met Ser Ser Ile Lys Ile Glu Cys Val Leu Arg Glu Asn Tyr Arg Cys
 37 1 5 10 15
 39 ggg gag tcc cct gtg tgg gag gag gca tca aag tgt ctg ctg ttt gta 96
 40 Gly Glu Ser Pro Val Trp Glu Ala Ser Lys Cys Leu Leu Phe Val
 41 20 25 30
 43 gac atc cct tca aag act gtc tgc cga tgg gat tcg atc agc aat cga 144
 44 Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
 45 35 40 45
 47 gtg cag cga gtt ggt gta gat gcc cca gtc agt tca gtg gca ctt cga 192
 48 Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
 49 50 55 60
 51 cag tca gga ggc tat gtt gcc acc att gga acc aag ttc tgt gct ttg 240
 52 Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
 53 65 70 75 80
 55 aac tgg gaa gat caa tca gta ttt atc cta gcc atg gtg gat gaa gat 288
 56 Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
 57 85 90 95
 59 aag aaa aac aat cga ttc aat gat ggg aag gtg gat cct gct ggg aga 336
 60 Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
 61 100 105 110
 63 tac ttt gct ggt acc atg gct gag gaa acc gcc cca gct gtt ctg gag 384



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64 Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
 65 115 120 125
 67 cgg cac caa ggg tcc ttg tac tcc ctt ttt cct gat cac agt gtg aag 432
 68 Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
 69 130 135 140
 71 aaa tac ttt aac caa gtg gat atc tcc aat ggt ttg gat tgg tcc ctg 480
 72 Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
 73 145 150 155 160
 75 gac cat aaa atc ttc tac tac att gac agc ctg tcc tac act gtg gat 528
 76 Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
 77 165 170 175
 79 gcc ttt gac tat gac ctg cca aca gga cag att tcc aac cgc agg act 576
 80 Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
 81 180 185 190
 83 gtt tac aag atg gaa aaa gat gaa caa atc cca gat gga atg tgc att 624
 84 Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
 85 195 200 205
 87 gat gtt gag ggg aag ctt ttg gtg gcc tgt tac aat gga gga aga gta 672
 88 Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
 89 210 215 220
 91 att cgc cta gat cct gag aca ggg aaa aga ctg caa act gtg aag ttg 720
 92 Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
 93 225 230 235 240
 95 cct gtt gat aaa aca act tca tgc tgc ttt gga ggg aag gat tac tct 768
 96 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
 97 245 250 255
 99 gaa atg tac gtg aca tgt gcc agg gat ggg atg agc gcc gaa ggt ctt 816
 100 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
 101 260 265 270
 103 ttg agg cag cct gat gct ggt aac att ttc aag ata aca ggt ctt ggg 864
 104 Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
 105 275 280 285
 107 gtc aaa gga att gct cca tat tcc tat gca ggg taa
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 109 290 295
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 119 1 5 10 15
 121 Gly Glu Ser Pro Val Trp Glu Glu Ala Ser Lys Cys Leu Leu Phe Val
 122 20 25 30
 124 Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
 125 35 40 45
 127 Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
 128 50 55 60
 130 Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu

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131 65 70 75 80
 133 Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
 134 85 90 95
 136 Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
 137 100 105 110
 139 Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
 140 115 120 125
 142 Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
 143 130 135 140
 145 Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
 146 145 150 155 160
 148 Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
 149 165 170 175
 151 Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
 152 180 185 190
 154 Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
 155 195 200 205
 157 Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
 158 210 215 220
 160 Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
 161 225 230 235 240
 163 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
 164 245 250 255
 166 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
 167 260 265 270
 169 Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
 170 275 280 285
 172 Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
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 190 <211> LENGTH: 23
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 192 <213> ORGANISM: Artificial Sequence
 194 <220> FEATURE:
 195 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 196 primer huRC-2
 198 <400> SEQUENCE: 4
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VERIFICATION SUMMARY

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